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CHRISTENSON, STEVEN D.
STANDAGE, SCOTT

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ANTIBIOTIC C-1027

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<140> 09/478,188
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<210> 6
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<220>
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<210> 7
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tcagacggcg gaggg   15

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gtgacagcag tcaag                                              15


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<400> 22
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<400> 23
gtggagtact ggaac                                              15


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ctacagccct ccgag   15

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atgtcttcaa cccgt   15

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atgaaggcac ttgta   15

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tcaggccgcg atctc   15

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<210> 46
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tcacgtggtg atggc                                              15


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gtgcgtccct tccgt   15

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tcatacggcg gcgcc                                                    15


<210> 59
<211> 15
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<220>
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<400> 59
gtgagcgcac aactc                                                    15


<210> 60
<211> 15
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<220>
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<400> 60
tcacggctgt gcctg                                                    15


<210> 61
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<220>
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<400> 61
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<210> 62
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<220>
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<210> 63
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<400> 63
atgacgacgt ccgac                                                    15


<210> 64
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<220>
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<400> 64
tcaggaggtg aaggg                                                    15


<210> 65
<211> 15
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<220>
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atggcattga ctcaa                                                    15


<210> 66
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<220>
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<210> 67
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<210> 68
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<220>
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<400> 68
tcagcgggtg agccg                                                    15


<210> 69
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<400> 69
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<210> 70
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<220>
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<400> 70
tcactgcgtt ccgga                                                    15


<210> 71
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<400> 71
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<210> 72
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<400> 72
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gtgttgggcg atgaggac   18

<210> 74
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<220>
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tcagaccgcg gacatctg   18

<210> 75
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<213> Artificial Sequence

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atggccggcc tggtcatg   18

<210> 76
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<213> Artificial Sequence

<220>
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<400> 76
tcaggacccg agggtcac   18

<210> 77
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<220>
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gtggaccaga cgtctacg   18

<210> 78
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<220>
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<400> 78
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<210> 79
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<220>
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<210> 80
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<210> 83
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<400> 83
gtgtatcagc cggactgt                                              18


<210> 84
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<400> 84
ctactcattc cagttgtg                                              18


<210> 85
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<400> 85
atgtctacgg gctatctc                                              18


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atgttctccc ccgccgcc   18

<210> 88
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<400> 88
tcagtacgcc tggtgggc   18

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atgaattcgc tcgacgac   18

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tcagctcccg gtcgccgc   18

<210> 91
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atgaccgcga cgaatcct   18

<210> 92
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ctaggcggcg cgtcccgc   18

<210> 93
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<210> 94
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tcagccgcgc gccgacgg   18

<210> 95
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<400> 95
atgaccctgg aggcctac   18

<210> 96
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<400> 96
gtgaaaagtg actctgcc   18

<210> 97
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<400> 97
gtgaccacga acaccatc   18

<210> 98
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<400> 98
tcatgcgggg ctcccggt   18

<210> 99
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<400> 99
tcaacggcga gttggctg   18

<210> 100
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<400> 100
tcacccgcga tctcgatc   18

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<220>
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tcacctcgcc gtactcac                                                18
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<210> 102
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<212> DNA
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<220>
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<400> 102
agctccatca agtcsatgrt cgg                                          23


<210> 103
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<220>
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<400> 103
ccggtgttsa csgcgtagaa ccaggcg                                      27
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<400> 104
gacacvgcnt gytcbtcv                                                18


<210> 105
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<220>
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rtgsgcrttv gtnccrct   18

<210> 106
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<220>
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<400> 106
gcstcccgsg acctgggctt cgactc   26

<210> 107
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<220>
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<400> 107
agsgasgasg agcaggcggt stcsac   26

<210> 108
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<400> 108
csggsgssgc sggsttcatc gg   22

<210> 109
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<220>
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<400> 109
gggwrctggy rsggsccgta gttg   24

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<220>
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aggtggaggc gctcaccgag                                              20


<210> 111
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<220>
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gggcgtcagg ccgtaagaag                                              20


<210> 112
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<220>
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<222> (101)..(1096)
<223> sgcA gene

<220>
<221> CDS
<222> (1143)..(2705)
<223> sgcB gene

<400> 112
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aactgacgaa gcgtcatcgc cgtgacaagg aggcggaccg atg agg atg ctg gtg    115
                                                Met Arg Met Leu Val
                                                1                5


acg ggc gga gcg ggt ttc atc ggc tcg cag ttc gtg cgg gcc aca ctg    163
Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe Val Arg Ala Thr Leu
                10                  15                  20


cac ggc gag ctg ccg ggt tcc gag gac gcc cgg gtg acg gtc ctg gac    211
His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg Val Thr Val Leu Asp
                25                  30                  35


aag ctg acg tac tcc ggc aat ccg gcc aac ctc acc tcc gtc gcg gcc    259
Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu Thr Ser Val Ala Ala
                40                  45                  50
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cat ccg cgg tac acc ttc gtc cag ggc gac acc gtc gac ccg cgc gtc    307
His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr Val Asp Pro Arg Val
    55                  60                  65

gtc gac gag gtg gtc gcc ggc cac gac gtc atc gtc cac ttc gcg gcg    355
Val Asp Glu Val Val Ala Gly His Asp Val Ile Val His Phe Ala Ala
70                  75                  80                  85

gag tcg cac gtg gac cgc tcg atc gac acc gcc acc cgg ttc gtc acg    403
Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala Thr Arg Phe Val Thr
            90                  95                  100

acc aac gtg ctc ggg acc cag acg ctg ctg gaa gcg gct ctc cgg cac    451
Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu Ala Ala Leu Arg His
            105                 110                 115

ggg gtc ggc cgg ttc gtg cac gtg tcg acc gac gag gtc tac ggg tcg    499
Gly Val Gly Arg Phe Val His Val Ser Thr Asp Glu Val Tyr Gly Ser
            120                 125                 130

atc gcc tcc ggc tca tgg acc gag gac acc ccg ctc gcc ccc aac gtc    547
Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro Leu Ala Pro Asn Val
    135                 140                 145

ccc tac gcg gcg tcg aag gcg ggt tcg gac ctg atg gcg ctc gcc tgg    595
Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu Met Ala Leu Ala Trp
150                 155                 160                 165

cac cgc acc cgg ggc ctg gac gtc gtc gtc acc cgg tgc acc aac aac    643
His Arg Thr Arg Gly Leu Asp Val Val Val Thr Arg Cys Thr Asn Asn
            170                 175                 180

tac ggt ccc tac cag tac ccc gag aag gtg atc ccg ctc ttc gtc acc    691
Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile Pro Leu Phe Val Thr
            185                 190                 195

aac atc ctc gac ggc ttg cgg gtg ccc ctg tac ggg gac ggc gcc cac    739
Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr Gly Asp Gly Ala His
            200                 205                 210

cgc cgg gac tgg ctg cac gtg tcc gac cac tgc cgg gcc atc cag atg    787
Arg Arg Asp Trp Leu His Val Ser Asp His Cys Arg Ala Ile Gln Met
    215                 220                 225

gtc atg aac tcc ggc cgg gcc ggg gag gtc tac cac atc ggc ggc ggc    835
Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr His Ile Gly Gly Gly
230                 235                 240                 245

acc gaa ctc tcc aac gag gaa ctc acc ggc ctg ttg ctc acg gcg tgc    883
Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu Leu Leu Thr Ala Cys
            250                 255                 260

ggc acc gac tgg tcc tgc gtg gac cgg gtg gcc gac cgg cag ggg cac    931
Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala Asp Arg Gln Gly His
            265                 270                 275
```

```
gac cgc cgc tac tcg ctc gac atc acg aag atc cgg cag gaa ctg ggc    979
Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile Arg Gln Glu Leu Gly
        280                 285                 290

tac gag ccc ctg gtc gcc ttc gag gac ggc ctg gcc gcg acg gtg aag   1027
Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu Ala Ala Thr Val Lys
    295                 300                 305

tgg tac cac gag aac cgt tcg tgg tgg cag ccg ctg aag gaa gcg gcc   1075
Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro Leu Lys Glu Ala Ala
310                 315                 320                 325

ggc ctc ctg gac gcc gtc ggc tgacggcagc caccgctagg aacaccccag      1126
Gly Leu Leu Asp Ala Val Gly
            330

gaaaggagcc acctcc gtg aca gca gtc aag gag ccg acg tcc cgc gca gga 1178
                  Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly
                        335                 340

cgg cgg gag tgg atc gct ctc gtc gtc ctc tcc ttg ccc acg atg ctg   1226
Arg Arg Glu Trp Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu
345                 350                 355                 360

ttg atg ctg gac atc aac gtc ctc atg ctg gcc ttg ccg cag ttg agc   1274
Leu Met Leu Asp Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser
            365                 370                 375

gag gat ctc ggc gcg agc agc acg caa cag ctg tgg atc acc gac atc   1322
Glu Asp Leu Gly Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile
            380                 385                 390

tac gga ttc gcg atc gcc ggc ttc ctg gtg acc atg ggc acc ctc ggc   1370
Tyr Gly Phe Ala Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly
        395                 400                 405

gac cgg atc ggc cgc cgc agg ctc ctg ctc ggg ggc gcg gcc gtc ttc   1418
Asp Arg Ile Gly Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe
        410                 415                 420

gcg gtc gtg tcc gtc gtc gcc gcg ttc tcc gac agc gcg gcg atg ctc   1466
Ala Val Val Ser Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu
425                 430                 435                 440

gtc gtc agc cgc gcc gtg ctc ggc gtc gcc ggg gcc acg gtg atg ccc   1514
Val Val Ser Arg Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro
            445                 450                 455

tcg acg ctc gcg ctc atc agc aac atg ttc gag gac ccc aag gag cgg   1562
Ser Thr Leu Ala Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg
            460                 465                 470

ggc acc gcc atc gcc atg tgg gcg agc gcc atg atg gcc gga gtc gcc   1610
Gly Thr Ala Ile Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala
            475                 480                 485
```

```
ctc ggg ccc gcc gtc ggc ggc ctg gtc ctc gcc gcg ttc tgg tgg gga    1658
Leu Gly Pro Ala Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly
    490                     495                 500

tcg gtg ttc ctc atc gcc gtt ccg gtg atg ctg ctg gtg gtg gtc acc    1706
Ser Val Phe Leu Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr
505                     510                 515                 520

ggc ccc gtg ctg ctc acc gag tcc cgc gac ccg gac gcc gga cgg ctg    1754
Gly Pro Val Leu Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu
                525                 530                 535

gac ctg ctg agc gcg ggg ctc tcc ctc gcg acc gtg ctg ccg gtg atc    1802
Asp Leu Leu Ser Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile
            540                 545                 550

tac gga ctg aag gag ctg gcc cgg acc ggg tgg gac ccg ctc gcc gcc    1850
Tyr Gly Leu Lys Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala
            555                 560                 565

ggc gcg gtg gtc ctc ggc gtg atc ttc ggc gcg ctg ttc gtc cag cgc    1898
Gly Ala Val Val Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg
    570                 575                 580

cag cgg cgg ttg gcc gac ccc atg ctg gac ctc ggc ctc ttc gcc gac    1946
Gln Arg Arg Leu Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp
585                 590                 595                 600

cgc acc ctg cgg gcg ggt ctg acg gtc agt ctg gtc aac gcc gtc atc    1994
Arg Thr Leu Arg Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile
                605                 610                 615

atg ggc ggg acc gga ctg atg gtc gcc ctg tac ctc cag acg atc gcc    2042
Met Gly Gly Thr Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala
            620                 625                 630

ggt cac tcc ccg ttg gcc gcc ggg ctg tgg ctg ctg atc ccg gcc tgc    2090
Gly His Ser Pro Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys
            635                 640                 645

atg ctc gtc gtg ggc gta cag ctg tcg aac ctg ctg gcc cag cgg atg    2138
Met Leu Val Val Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met
    650                 655                 660

ccc cct tcc cgg gtg ctg ctg ggg gga ctg ctg atc gcg gcc gtc gga    2186
Pro Pro Ser Arg Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly
665                 670                 675                 680

cag ctc ctg atc acc cag gtg gac acc gag gac acc gcc ctc ctc atc    2234
Gln Leu Leu Ile Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile
                685                 690                 695

gcg gcc acc acc ctg atc tac ttc ggc gcc tca ccg gtg ggg ccg atc    2282
Ala Ala Thr Thr Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile
            700                 705                 710
```

```
acc acg ggc gcg atc atg gga gcc gcg ccc ccg gag aag gcg ggt gcc    2330
Thr Thr Gly Ala Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala
        715             720             725

gcc tcg tcg ctg tcc gcc acc ggc ggc gag ttc gga gtg gcg ctc ggc    2378
Ala Ser Ser Leu Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly
    730             735             740

atc gcg ggc ctg ggg agt ctg ggc acc gtc gtg tac agc gcc ggg gtc    2426
Ile Ala Gly Leu Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val
745             750             755             760

gag gtg ccg gac gcg gcc ggg ccc gcc gac gcc gac gcc gcg cag gag    2474
Glu Val Pro Asp Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu
            765             770             775

agc atc gcc ggc gcc ctg cac acg gcc ggt cag ctg gca ccg ggc agc    2522
Ser Ile Ala Gly Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser
            780             785             790

gcc gac gcc ctg ctg gac tcc gcg cgc gcg gcc ttc acc agc ggc gtg    2570
Ala Asp Ala Leu Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val
        795             800             805

cag tcc gtc gcc gcc gtc tgc gcc gtg ttc tcc ctg gcg ctc gcc gtc    2618
Gln Ser Val Ala Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val
    810             815             820

ctc atc ggc acc cgg ctg cgg gac att tcc gcg atg gac cac ggg cac    2666
Leu Ile Gly Thr Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His
825             830             835             840

ggc gag gaa ccg gcc gag aac gac gct caa ccg gcc aca tgagcgcact    2715
Gly Glu Glu Pro Ala Glu Asn Asp Ala Gln Pro Ala Thr
            845             850
```

```
tccggagatg caacggccgc cgtcgaggta tgaggatcac cttccggggt gcacctgcac 2775

ggcaacggag gcgtagtgga gtactggaac agcacggcgg agaccatgcc ccgccaggaa 2835

ctcgaacagt ggaagtggcg caggctccag gccgccatgg accacgccag aaggctttcg 2895

cccttctggc gggaacgact ccccgagaac atcacctcca tggcggacta cgcggcgcgg 2955

gtgcctctcc tgcgcaaggc cgacctcctc gccgcggaag ccgcgtctcc cccttacggc 3015

acctggccct cgctggatcc                                             3035
```

```
<210> 113
<211> 332
<212> PRT
<213> Streptomyces globisporus

<220>
<223> sgcA
```

<400> 113

```
Met Arg Met Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe
  1               5              10              15

Val Arg Ala Thr Leu His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg
            20              25              30

Val Thr Val Leu Asp Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu
            35              40              45

Thr Ser Val Ala Ala His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr
    50              55              60

Val Asp Pro Arg Val Val Asp Glu Val Val Ala Gly His Asp Val Ile
 65              70              75              80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala
                85              90              95

Thr Arg Phe Val Thr Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu
            100             105             110

Ala Ala Leu Arg His Gly Val Gly Arg Phe Val His Val Ser Thr Asp
        115             120             125

Glu Val Tyr Gly Ser Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro
    130             135             140

Leu Ala Pro Asn Val Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu
145             150             155             160

Met Ala Leu Ala Trp His Arg Thr Arg Gly Leu Asp Val Val Val Thr
            165             170             175

Arg Cys Thr Asn Asn Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile
        180             185             190

Pro Leu Phe Val Thr Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr
        195             200             205

Gly Asp Gly Ala His Arg Arg Asp Trp Leu His Val Ser Asp His Cys
    210             215             220

Arg Ala Ile Gln Met Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr
225             230             235             240

His Ile Gly Gly Gly Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu
            245             250             255

Leu Leu Thr Ala Cys Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala
        260             265             270

Asp Arg Gln Gly His Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile
        275             280             285

Arg Gln Glu Leu Gly Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu
    290             295             300
```

```
Ala Ala Thr Val Lys Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro
305             310             315             320

Leu Lys Glu Ala Ala Gly Leu Leu Asp Ala Val Gly
            325             330
```

<210> 114
<211> 521
<212> PRT
<213> Streptomyces globisporus

<220>
<223> sgcB

<400> 114
```
Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly Arg Arg Glu Trp
  1             5               10              15

Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu Leu Met Leu Asp
            20              25              30

Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser Glu Asp Leu Gly
        35              40              45

Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile Tyr Gly Phe Ala
    50              55              60

Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly Asp Arg Ile Gly
 65             70              75              80

Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe Ala Val Val Ser
            85              90              95

Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu Val Val Ser Arg
            100             105             110

Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro Ser Thr Leu Ala
        115             120             125

Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg Gly Thr Ala Ile
    130             135             140

Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala Leu Gly Pro Ala
145             150             155             160

Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly Ser Val Phe Leu
            165             170             175

Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr Gly Pro Val Leu
        180             185             190

Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu Asp Leu Leu Ser
    195             200             205

Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile Tyr Gly Leu Lys
    210             215             220
```

```
Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala Gly Ala Val Val
225              230              235              240

Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg Gln Arg Arg Leu
             245              250              255

Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp Arg Thr Leu Arg
             260              265              270

Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile Met Gly Gly Thr
             275              280              285

Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala Gly His Ser Pro
290              295              300

Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys Met Leu Val Val
305              310              315              320

Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met Pro Pro Ser Arg
             325              330              335

Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly Gln Leu Leu Ile
             340              345              350

Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile Ala Ala Thr Thr
             355              360              365

Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile Thr Thr Gly Ala
370              375              380

Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala Ala Ser Ser Leu
385              390              395              400

Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly Ile Ala Gly Leu
             405              410              415

Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val Glu Val Pro Asp
             420              425              430

Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu Ser Ile Ala Gly
         435              440              445

Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser Ala Asp Ala Leu
450              455              460

Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val Gln Ser Val Ala
465              470              475              480

Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val Leu Ile Gly Thr
             485              490              495

Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His Gly Glu Glu Pro
         500              505              510

Ala Glu Asn Asp Ala Gln Pro Ala Thr
         515              520
```

<210> 115
<211> 329
<212> PRT
<213> Saccharopolyspora erythraea

<400> 115

```
Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
 1               5                  10                  15

Val Arg Gln Leu Leu Gly Gly Ala Tyr Pro Ala Phe Ala Gly Ala Asp
                20                  25                  30

Val Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Glu Glu Asn Leu
             35                  40                  45

Arg Pro Val Ala Asp Asp Pro Arg Phe Arg Phe Val Arg Gly Asp Ile
         50                  55                  60

Cys Glu Trp Asp Val Val Ser Glu Val Met Arg Glu Val Asp Val Val
 65                  70                  75                  80

Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Leu Gly Ala
                 85                  90                  95

Ser Asp Phe Val Val Thr Asn Val Val Gly Thr Asn Thr Leu Leu Gln
            100                 105                 110

Gly Ala Leu Ala Ala Asn Val Ser Lys Phe Val His Val Ser Thr Asp
         115                 120                 125

Glu Val Tyr Gly Thr Ile Glu His Gly Ser Trp Pro Glu Asp His Leu
     130                 135                 140

Leu Glu Pro Asn Ser Pro Tyr Ser Ala Ala Lys Ala Gly Ser Asp Leu
145                 150                 155                 160

Ile Ala Arg Ala Tyr His Arg Thr His Gly Leu Pro Val Cys Ile Thr
                165                 170                 175

Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Val Leu
             180                 185                 190

Pro Leu Phe Ile Thr Asn Leu Met Asp Gly Arg Arg Val Pro Leu Tyr
         195                 200                 205

Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Thr Asp His Cys
     210                 215                 220

Arg Gly Ile Gln Leu Val Ala Glu Ser Gly Arg Ala Gly Glu Ile Tyr
225                 230                 235                 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Lys Glu Leu Thr Glu Arg
                245                 250                 255

Val Leu Glu Leu Met Gly Gln Asp Trp Ser Met Val Gln Pro Val Thr
             260                 265                 270
```

Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp His Thr Lys Ile
     275   280   285

Ser Glu Glu Leu Gly Tyr Glu Pro Val Val Pro Phe Glu Arg Gly Leu
     290   295   300

Ala Glu Thr Ile Glu Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305   310   315   320

Leu Lys Ser Ala Pro Asp Gly Gly Lys
         325

<210> 116
<211> 333
<212> PRT
<213> Streptomyces fradiae

<400> 116
Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
1   5   10   15

Thr Gly Gln Leu Leu Thr Gly Ala Tyr Pro Asp Leu Gly Ala Thr Arg
     20   25   30

Thr Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Pro Ala Asn Leu
     35   40   45

Glu His Val Ala Gly His Pro Asp Leu Glu Phe Val Arg Gly Asp Ile
     50   55   60

Ala Asp His Gly Trp Trp Arg Arg Leu Met Glu Gly Val Gly Leu Val
65   70   75   80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Ser Ser
         85   90   95

Glu Ala Phe Val Arg Thr Asn Val Glu Gly Thr Arg Val Leu Leu Gln
     100   105   110

Ala Ala Val Asp Ala Gly Val Gly Arg Phe Val His Ile Ser Thr Asp
     115   120   125

Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Pro Glu Asp His Pro
     130   135   140

Val Ala Pro Asn Ser Pro Tyr Ala Ala Thr Lys Lys Ala Ser Asp Leu
145   150   155   160

Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Asp Val Arg Val Thr
     165   170   175

Arg Cys Ser Asn Asn Tyr Gly Pro Arg Gln Tyr Pro Glu Lys Ala Val
     180   185   190

Pro Leu Phe Thr Thr Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr
     195   200   205

```
Gly Asp Gly Gly Asn Thr Arg Glu Trp Leu His Val Asp Asp His Cys
    210                 215                 220

Arg Gly Val Ala Leu Val Gly Ala Gly Gly Arg Pro Gly Val Ile Tyr
225                 230                 235                 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Ala Glu Leu Thr Asp Arg
                245                 250                 255

Ile Leu Glu Leu Cys Gly Ala Asp Arg Ser Ala Leu Arg Arg Val Ala
    260                 265                 270

Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
    275                 280                 285

Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
    290                 295                 300

Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305                 310                 315                 320

Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
                325                 330
```

<210> 117
<211> 331
<212> PRT
<213> Streptomyces argillaceus

<400> 117

```
Met Thr Thr Thr Ser Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly
1               5               10                  15

Ser His Tyr Val Arg Thr Leu Leu Gly Pro Arg Gly Val Pro Asp Val
            20                  25                  30

Thr Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Thr Leu Thr Asn
            35                  40                  45

Leu Ala Glu Val Ser Asp Ser Asp Arg Phe Arg Phe Val Arg Gly Asp
        50                  55                  60

Ile Cys Asp Ala Pro Leu Val Asp Asp Leu Leu Ala Val His Asp Gln
65                  70                  75                  80

Val Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Leu Gly
            85                  90                  95

Ala Ala Asp Phe Val Arg Thr Asn Val Thr Gly Thr Gln Thr Leu Leu
            100                 105                 110

Asp Ala Ala Leu Arg Gln Gly Ile Glu Thr Phe Val His Ile Ser Thr
        115                 120                 125

Asp Glu Val Tyr Gly Ser Ile Asp Ala Gly Ser Trp Pro Glu Thr Ala
    130                 135                 140
```

```
Pro Val Ser Pro Asn Ser Leu Tyr Ser Ala Ala Lys Ala Ser Ser Asp
145                 150                 155                 160

Leu Val Ala Leu Ala Tyr His Arg Thr His Gly Leu Asp Val Arg Val
                165                 170                 175

Thr Arg Cys Ser Asn Asn Tyr Gly Ser His Gln Phe Pro Glu Lys Val
                180                 185                 190

Ile Pro Leu Phe Val Thr Ser Leu Leu Asp Gly Arg Glu Val Pro Leu
            195                 200                 205

Tyr Gly Asp Gly Thr Asn Val Arg Asp Trp Leu His Val Asp Asp His
        210                 215                 220

Val Arg Ala Ile Glu Leu Val Arg Thr Gly Gly Arg Ala Gly Glu Val
225                 230                 235                 240

Tyr Asn Ile Gly Gly Gly Thr Glu Leu Ser Asn Lys Glu Leu Thr Gln
                245                 250                 255

Leu Leu Leu Asp Ala Cys Gly Ala Gly Trp Asp Arg Val Arg Tyr Val
            260                 265                 270

Thr Asp Arg Lys Gly His His Asp Arg Arg Tyr Ser Val Asp Cys Thr Lys
        275                 280                 285

Ile Arg Arg Glu Leu Gly Tyr Arg Pro Ala Arg Glu Phe Gly Asp Ala
        290                 295                 300

Leu Ala Glu Thr Val Ala Trp Tyr Arg His His Arg Ala Trp Trp Glu
305                 310                 315                 320

Pro Leu Thr Arg Ala Tyr Gly Ala Val Ala Ala
                325                 330
```

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 118
His His His His His His
 1   5